



SEQUENCE LISTING

<110> FUJITA, JUN

<120> GANKYRIN

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<140> 09/509,775

<141> 2000-03-31

<150> PCT/JP98/04467

<151> 1998-10-02

<150> JP 9-286214

<151> 1997-03-10

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 780

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(774)

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				Met	Glu	Gly	Cys	Val	Ser	
				1				5		

aac	cta	atg	gtc	tgc	aac	ctg	gcc	tac	agc	ggg	aag	ctg	gaa	gag	ttg	162
Asn	Leu	Met	Val	Cys	Asn	Leu	Ala	Tyr	Ser	Gly	Lys	Leu	Glu	Glu	Leu	
			10					15						20		

aag	gag	agt	att	ctg	gcc	gat	aaa	tcc	ctg	gct	act	aga	act	gac	cag	210
Lys	Glu	Ser	Ile	Leu	Ala	Asp	Lys	Ser	Leu	Ala	Thr	Arg	Thr	Asp	Gln	
		25					30					35				

gac	agc	aga	act	gca	ttg	cac	tgg	gca	tgc	tca	gct	gga	cat	aca	gaa	258
Asp	Ser	Arg	Thr	Ala	Leu	His	Trp	Ala	Cys	Ser	Ala	Gly	His	Thr	Glu	
		40				45					50					

att	gtt	gaa	ttt	ttg	ttg	caa	ctt	gga	gtg	cca	gtg	aat	gat	aaa	gac	306
Ile	Val	Glu	Phe	Leu	Leu	Gln	Leu	Gly	Val	Pro	Val	Asn	Asp	Lys	Asp	
	55				60				65						70	

gat	gca	ggt	tgg	tct	cct	ctt	cat	att	gcg	gct	tct	gct	ggc	cgg	gat	354
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Gly Lys Leu Glu Glu Leu Lys Glu Ser Ile Leu Ala Asp Lys Ser Leu
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Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
      35                    40                   45

Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
      50                    55                   60

Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
      65                    70                   75                   80

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Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Gly Lys Gly
85 90 95

Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
100 105 110

Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly
115 120 125

Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Glu Ala Thr Ala Met His
130 135 140

Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Ile His Ile Leu Leu Tyr
145 150 155 160

Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
165 170 175

His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val
180 185 190

Ser Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
195 200 205

Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Met Val
210 215 220

Glu Gly
225

<210> 3
<211> 696
<212> DNA
<213> Mus sp.

<220>
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<222> (1) .. (693)

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1 5 10 15

ggg aag ctg gat gag ttg aag gag cgc att ttg gct gat aaa tct ctg 96
Gly Lys Leu Asp Glu Leu Lys Glu Arg Ile Leu Ala Asp Lys Ser Leu
20 25 30

gct act aga act gat cag gac agc aga aca gct ttg cac tgg gca tgc 144
Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
35 40 45

tca gct ggc cat aca gaa att gtt gaa ttc ttg ctg caa ctt gga gtg	192
Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val	
50 55 60	
cca gtn aat gat aaa gat gac gca ggt tgg tct cct ctt cat att gct	240
Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala	
65 70 75 80	
gcc tcc gct ggc cgg gat gag att gta aaa gcc ctt ctg gtg aaa ggt	288
Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly	
85 90 95	
gca cat gtt aat tct gtc aat caa aac ggc tgc act cca ctc cat tat	336
Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr	
100 105 110	
gca gct tcg aag aat agg cat gag att tct gtt atg tta cta gaa ggt	384
Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly	
115 120 125	
ggg gct aac cca gat gcg aag gac cat tac gat gct aca gca atg cac	432
Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His	
130 135 140	
cgg gca gca gcc aag ggt aac ttg aag atg gtt cac atc ctt ctg ttc	480
Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe	
145 150 155 160	
tac aaa gca tcc aca aac atc caa gac act gag ggt aac act cct cta	528
Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu	
165 170 175	
cac tta gcc tgt gat gaa gag aga gtg gaa gag gca aaa ttt ctg gtg	576
His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val	
180 185 190	
act caa gga gca agt att tac att gag aat aaa gaa gaa aag aca ccc	624
Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro	
195 200 205	
ctg caa gtt gcc aaa ggg ggc ctg ggt tta ata ctc aag aga cta gca	672
Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala	
210 215 220	
gaa agt gaa gag gct tct atg tag	696
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 <213> Mus sp.

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 20 25 30
 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
 35 40 45
 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
 50 55 60
 Pro Val Asn Asp Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
 65 70 75 80
 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Val Lys Gly
 85 90 95
 Ala His Val Asn Ser Val Asn Gln Asn Gly Cys Thr Pro Leu His Tyr
 100 105 110
 Ala Ala Ser Lys Asn Arg His Glu Ile Ser Val Met Leu Leu Glu Gly
 115 120 125
 Gly Ala Asn Pro Asp Ala Lys Asp His Tyr Asp Ala Thr Ala Met His
 130 135 140
 Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe
 145 150 155 160
 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
 165 170 175
 His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Phe Leu Val
 180 185 190
 Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
 195 200 205
 Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Leu Ala
 210 215 220
 Glu Ser Glu Glu Ala Ser Met
 225 230

<210> 5
 <211> 696
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1) .. (693)

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ggg aag ctg gat gag ttg aag gaa agc att ttg gct gat aag tct ctg	96
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gcc act aga act gat cag gac agc aga aca gca ttg cac tgg gca tgc	144
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35 40 45	
tca gct ggt cat aca gaa att gtt gaa ttc ttg ctg caa ctt gga gtg	192
Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val	
50 55 60	
cca gta aat gaa aaa gac gat gca ggt tgg tct cct ctt cat att gct	240
Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala	
65 70 75 80	
gct tcc gct ggc cgg gat gag att gta aaa gcc ctt ctg ata aaa ggg	288
Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly	
85 90 95	
gca caa gtg aat gcc gtc aat cag aat ggc tgc acg gcc ctt cat tat	336
Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr	
100 105 110	
gca gct tcc aag aat agg cat gag att gct gtt atg tta cta gaa ggt	384
Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly	
115 120 125	
ggg gct aat cca gat gct aag aac cat tat gat gct aca gca atg cac	432
Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His	
130 135 140	
cgg gca gca gcc aag ggt aac ttg aag atg gtt cat atc ctt ctg ttc	480
Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe	
145 150 155 160	
tac aaa gca tcc aca aac atc caa gat act gag ggt aac act cct cta	528
Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu	
165 170 175	
cac tta gcc tgt gat gag gag aga gtg gaa gaa gca aaa ttg ctg gtg	576
His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val	
180 185 190	
acc caa gga gca agt att tac att gaa aat aag gaa gaa aag aca ccg	624
Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro	
195 200 205	
ctg caa gtc gcc aaa ggg ggc ctg ggt tta ata ctc aaa aga atc gca	672
Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Ala	
210 215 220	
gaa agt gaa gag gct tct atg tag	696
Glu Ser Glu Glu Ala Ser Met	
225 230	

<210> 6
 <211> 231
 <212> PRT
 <213> Rattus sp.

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 20 25 30
 Ala Thr Arg Thr Asp Gln Asp Ser Arg Thr Ala Leu His Trp Ala Cys
 35 40 45
 Ser Ala Gly His Thr Glu Ile Val Glu Phe Leu Leu Gln Leu Gly Val
 50 55 60
 Pro Val Asn Glu Lys Asp Asp Ala Gly Trp Ser Pro Leu His Ile Ala
 65 70 75 80
 Ala Ser Ala Gly Arg Asp Glu Ile Val Lys Ala Leu Leu Ile Lys Gly
 85 90 95
 Ala Gln Val Asn Ala Val Asn Gln Asn Gly Cys Thr Ala Leu His Tyr
 100 105 110
 Ala Ala Ser Lys Asn Arg His Glu Ile Ala Val Met Leu Leu Glu Gly
 115 120 125
 Gly Ala Asn Pro Asp Ala Lys Asn His Tyr Asp Ala Thr Ala Met His
 130 135 140
 Arg Ala Ala Ala Lys Gly Asn Leu Lys Met Val His Ile Leu Leu Phe
 145 150 155 160
 Tyr Lys Ala Ser Thr Asn Ile Gln Asp Thr Glu Gly Asn Thr Pro Leu
 165 170 175
 His Leu Ala Cys Asp Glu Glu Arg Val Glu Glu Ala Lys Leu Leu Val
 180 185 190
 Thr Gln Gly Ala Ser Ile Tyr Ile Glu Asn Lys Glu Glu Lys Thr Pro
 195 200 205
 Leu Gln Val Ala Lys Gly Gly Leu Gly Leu Ile Leu Lys Arg Ile Ala
 210 215 220
 Glu Ser Glu Glu Ala Ser Met
 225 230

<210> 7
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 <212> PRT
 <213> Homo sapiens

<220>
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<210> 9
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<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<210> 10
<211> 28
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<213> Artificial Sequence
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<220>
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<223> L, I or V
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<220>  
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<222> (8)  
<223> A or S
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<220>
<221> MOD_RES
<222> (9)
<223> R, Q or K

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<220>

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<223> G or N

<220>
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<223> H or N

<220>
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<222> (12)
<223> V, L or T

<220>
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<222> (13)
<223> E or D

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<222> (14)
<223> V, I or M

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<223> V or A

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<223> K, E or R

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<222> (17)
<223> L or V

<220>
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<223> D, K, Q or E

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<223> D, N or S

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<223> V, P or I

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<223> N or D

<220>
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 <222> (27)
 <223> T, D or N

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 1 5 10 15
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 20 25

<210> 11
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <223> ankyrin repeat

<400> 11
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 1 5 10 15
 Ile Val Glu Phe Leu Leu Gln Leu Gly Val Pro Val Asn Asp Lys Asp
 20 25 30

Asp

<210> 12
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <223> ankyrin repeat

<400> 12
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 1 5 10 15
 Ile Val Lys Ala Leu Leu Gly Lys Gly Ala Gln Val Asn Ala Val Asn
 20 25 30

Gln

<210> 13
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <223> ankyrin repeat

<400> 13

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Ile Ala Val Met Leu Leu Glu Gly Gly Ala Asn Pro Asp Ala Lys Asp
 20 25 30

His

<210> 14

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

<400> 14

Tyr Glu Ala Thr Ala Met His Arg Ala Ala Ala Lys Gly Asn Leu Lys
 1 5 10 15

Met Ile His Ile Leu Leu Tyr Tyr Lys Ala Ser Thr Asn Ile Gln Asp
 20 25 30

Thr

<210> 15

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

<400> 15

Glu Gly Asn Thr Pro Leu His Leu Ala Cys Asp Glu Glu Arg Val Glu
 1 5 10 15

Glu Ala Lys Leu Leu Val Ser Gln Gly Ala Ser Ile Tyr Ile Glu Asn
 20 25 30

Lys

<210> 16

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<223> ankyrin repeat

<400> 16

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 1 5 10 15

Leu Lys Arg Met Val Glu Gly
 20